



# Assessment of genetic variability and heritability estimates in F<sub>2</sub> populations of bread wheat (*Triticum aestivum* L.)

Mir Muhammad Nizamani<sup>1</sup>✉, Feroz Gul Nizamani<sup>2</sup>, Raza Ali Rind<sup>2</sup>, Aamir Ali khokhar<sup>1</sup>

<sup>1</sup>Hainan Key Laboratory for Sustainable Utilization of Tropical Bioresources, Institute of Tropical Agriculture and Forestry, Hainan University, Haikou, China

<sup>2</sup>Department of Plant Breeding and Genetics, Sindh Agriculture University Tandojam, Pakistan

## ✉Corresponding author

Hainan Key Laboratory for Sustainable Utilization of Tropical Bioresources, Institute of Tropical Agriculture and Forestry, Hainan University, Haikou, China

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## General Note



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## ABSTRACT

Wheat breeders are working to increase the yield potential of bread wheat by developing new varieties with ideal genetic makeup to overcome the increasing consumption pressure of the population. To solve this problem, eight F<sub>2</sub> populations and six parents were studied during the years 2015-16. Analysis of variance revealed significant differences between the genotypes, hybrids, and parents vs hybrids for all traits studied. These results mark the further development value of breeding materials. Current research indicates

that the  $F_2$  population outperforms its parents on all traits studied based on average performance. This means that there is a transgressive segregator in the  $F_2$  population. If the selection of such potential plants is successful, they can be used to further improve bread wheat. The genetic parameters of  $F_2$  progenies indicated that cross TJ-83 x TD-1 displayed higher heritability estimates coupled with more genetic gains for plant height, spike length, spikelets per spike and grains per spike; TJ-83 x Sarsabz for tillers per plant and biological yield; TJ-83 x Moomal for peduncle length, grain yield per plant and harvest index and Moomal x TD-1 for seed index.

**Keywords:** Genetic advance, Genetic variability, Heritability, wheat

## 1. INTRODUCTION

Wheat breeders are emphasizing the potential to increase the yield of bread wheat by developing new varieties with the desired genetic makeup to overcome the increasing consumption pressure of the population [1]. Therefore, the increase in production and output is still the main goal of the prehistoric period and current breeding programs. Genetic manipulation of plant traits is the best way to increase wheat yield [2,3]. Grain yield is a product of many yield components, including most economic characteristics. Yield components and their inherent physiological mechanisms interact with crop growth environments and management practices to increase grain yield  $ha^{-1}$ . The researchers found significant differences in the bread wheat genotypes of the yield components [4,5]. This variation in yield between varieties indicates that there is a genetic variation between wheat varieties, which is responsible for the success of the breeding program [6]. Among other reasons, food production is strongly influenced by many genetic factors and environmental fluctuations [7].

The heritability estimate determines the extent to which a character is passed from one generation to the next and is a more valuable genetic attribute used with other parameters to predict genetic gain after a particular feature selection [8]. It is speculated that the higher the estimate of heritability, the simpler the selection procedure [9]. It has been emphasized that hereditary power alone is not sufficient to substantially improve the overall selection of late generations unless accompanied by substantial genetic advancement [10]. Estimates of heritability and genetic progression provide parents with knowledge of the inheritance of their offspring and their response to selection. Heritability and genetic progression values help breeders make choices more effective and predict choice responses [11]. For this purpose, genetic information about yield and its components is important for breeders to select and develop new and high yield cultivars. This is why selective genetic manipulation becomes extremely important [12]. In order to select the desired genotype, knowledge of the extent of gene action and variation in the breeding material is important for successful breeding programs [13,14]. In the wheat yield improvement program, the selection based on phenotypic variation is not efficient unless the genetic variation of the breeding material is fully evaluated and utilized. Therefore, it is necessary to obtain information on phenotypic and genotypic differences, hereditary and genetic progression. Several studies conducted at different locations in Ethiopia assessed genetic variability between tested bread wheat genotypes [1,4]. Therefore, this study aimed to study the heritability of  $F_2$  progeny yield and its components, and to understand how much phenotypic differences have been passed on to future generations. Therefore, the purpose of this study was to estimate the heritability in the broad sense and the genetic progress of the bread wheat  $F_2$  population to obtain yield and yield-related traits.

## 2. MATERIALS AND METHODS

Eight  $F_2$  populations along with their six parent's viz. Sunhri, PBGST-2, Sarsabz, TD-1, TJ-83 and Moomal were grown in the growing season of 2015-16. The experiment was carried-out in Randomized Complete Block Design with four replications. At maturity, fifteen plants per genotype from each replication were randomly tagged as treated index plants for recording the data on plant height (cm), peduncle length (cm), Tillers per plant, spike length (cm), Spikelets per pike, Grains per spike, seed index (1000 grain wt, g), Grain yield per plant (g), biological yield (g) and harvest index (%). The data were analyzed according to statistical technique outlined by Gomez and Gomez [15] through Statistix 8.1 computer software so as to work-out the differences among the genotypes for various traits. The genetic, phenotypic, environmental variances, broad sense heritability ( $h^2$ ) and expected response to selection were estimated according to procedure adopted by Baloch et al. [16]. All the inputs given and cultural practices were done according to the recommendations of the wheat crop.

### 3. RESULTS

#### Analysis of variance

The genetic improvement of any crop species depends on the size of the genetic variation and the heritability of the yield and its contribution characteristics. The purpose of this study was to assess the genetic variance, generalized heritability, and genetic progression under the 20% selection pressure of the wheat  $F_2$  population, which is 10 important traits. The results regarding the genetic parameters are listed in Tables 3 to 12. The analysis of variance in Table 1 reveals significant differences between the parents of all traits studied and the  $F_2$  population, indicating the presence of genetic variability between the parent and its  $F_2$  progeny. The characteristics of the study were: plant height, spike length, tillers per plant, ear length, spikelet per spike, Grains per spike, seed index (1000-grain weight), grain yield per plant, biomass yield per plant and harvest index. After finding that the mean square differences are significantly different, the data is further processed to determine genetic parameters. Researchers also found significant differences in various polygenic traits of the bread wheat genotype (*Triticum aestivum* L.) [17]. The average performance of the parent and  $F_2$  hybrids shown in Table 2. In Tables 3 to 12 their genetic parameters are presented.

**Table 1** Mean squares from analysis of variance for various quantitative traits in wheat genotypes

Traits	Replication	Genotypes	Parents (P)	$F_2$ hybrids (H)	P vs. H	Error
	(D.F= 3)	(D.F= 13)	(D.F= 5)	(D.F= 7)	(D.F= 1)	(D.F= 39)
Plant height	11.241	433.840**	905.262**	80.730**	548.501**	3.845
Peduncle length	2.079	78.088**	131.867**	15.318**	248.579**	0.837
Tillers per plant	0.005	0.703**	0.742**	0.587**	1.323**	0.037
Spike length	0.163	4.610**	4.247**	1.829**	25.889**	0.139
Spikelets per pike	0.494	14.033**	20.209**	5.391**	43.645**	0F.397
Grains per spike	7.763	77.428**	127.900**	41.037**	79.801**	6.608
Seed index	3.780	60.231**	81.856**	21.931**	216.786**	3.593
Grain yield per plant	3.200	7.872**	6.227**	2.22**	55.677**	0.721
Biological yield per plant	16.146	32.717**	31.326**	15.23**	162.044**	3.726
Harvest index	3.632	53.724**	47.986**	41.61**	167.212**	6.131

\*\*, = Significant at 1% probability level.

#### Mean performance of parents and their $F_2$ progenies

The average performance of the different traits of the 6 parents and their 8  $F_2$  populations is shown in Table 2. The results indicate that for most of the studied traits, the  $F_2$  progeny gave an average higher than their parental mean. The parental line TD-1 showed the smallest plants (57.50 cm), while Sarsabz produced the tallest plants (102.27 cm) compared to the other parents. In the  $F_2$  progeny, the shortest plant (76.65 cm) was observed in the cross TD-1 x Sarsabz, while the TJ-83 x Sarsabz produced the highest plant (90.47 cm), followed by Moomal x TD-1 (89.75 cm). In the parental line, the lower peduncle length was measured in TD-1 (25.88), followed by TJ-83 (26.00 cm), and the highest value was given by Sarsabz (39.56 cm). The offspring TD-1 x Sarsabz showed the lowest value (33.72). The highest value was shown by TJ-83 x Sarsabz (39.69 cm), followed by Sarsabz x Moomal (38.20). The maximum is the tiller produced by the parent TD-1 (5.66), followed by PGB-02 (5.25), and the minimum tiller is observed in Moomal (4.40). From the offspring, Sunhari x TD-1 (5.93) produced the most bifurcation, followed by TJ-83 x Sarsabz (5.66), while the minimum bifurcation was generated by TJ-83 x Moomal and TJ-83 x TD-1 (4.85). of. ). In the parent, the maximum ear length (12.97 cm) recorded in PBGST-2 was obtained from Sarsabz (12.40 cm), and the smallest spike was measured by TD-1 (10.28). In hybridization, the highest value of ear length was recorded by TJ-83 x Moomal (13.85 cm), and the second highest value was recorded in PGB-02 x TD-1 (13.22 cm). The lowest value was crossed by Sunhari x TD-1 recording (12.01 cm). The results further show that the largest spikelets per ear are noted in Sarsabz (21.70), followed by PBGST-2 (19.10), and the minimum of TD-1 (15.3) in the parents. The  $F_2$  hybrid Sarsabz x Moomal (20.82) is the highest level in hybridization, followed by almost Moomal x TD-1 (20.77), and a small value of this trait was observed in the cross TD-1 x Sarsabz (17.47). The variety Moomal produced the largest number of grains per panicle (63.04), the combined results were the same as Sarsabz (63.00), and TD-1 (49.38) was the smallest. Hybrid Moomal x TD-1 (64.07) calculates the maximum particle size for each ear, followed by Sarsabz x Moomal (63.20), and the minimum is derived

from two hybrids TJ-83 x Moomal and TD-1 x Sarsabz (55.37). The parental line PBGST-2 weighted highest seed index (37.08g), then TD-1 (31.17g), the lowest is given by Sarsabz (26.67g). The maximum seed index in the isolated population was weighted by PBGST-2 x TD-1 (37.50 g), weighted by Moomal x TD-1 (35.83 g), and recorded by Sunhari x TD-1 (30.41 g) value. For the trait yield per plant, the maximum kernel weight was observed in the parental PBGST-2 (7.70 g), followed by Sarsabz (7.53 g), and the minimum kernel weight was recorded in Moomal (4.77 g). The progeny from Moomal x TD-1 (9.52g) showed the maximum grain yield per plant, followed by TJ-83 x Moomal (8.82g), and TJ-83 x TD-1 and TD-1 x Sarsabz produced the smallest but similar yield (7.35, 7.37g). Regarding the biomass yield per plant, Sarsabz produced a maximum (21.31 g), followed by PBGST-2 (18.03 g), while Moomal produced 13.77 g. The offspring Moomal x TD-1 produced the maximum harvest index (22.05%), followed by two F<sub>2</sub> hybrids, such as Sunhari x TD-1, TJ-83 x Sarsabz (21.55, 21.49%), and the minimum value was expressed in TD-1 x Sarsabz. In the parental line, PBGST-2 had the highest (43.16%) harvest index, Sunhari (40.59%) ranked second, and TJ-83 (33.94%) had the lowest. The highest percentage of the harvest index came from the cross TJ-83 x Moomal (46.97%), then the cross TD-1 x Sarsabz (45.21%), and the lowest from TJ-83 x Sarsabz (38.18%).

**Table 2** Mean performance of parents and F<sub>2</sub> populations of wheat for plant height (cm), peduncle length (cm), Tillers per plant, spike length (cm) and spikelets spike, Grains per spike, seed index (g), Grain yield per plant (g), Biological yield per plant (g) and harvest index

Genotypes (Parents and F <sub>1</sub> hybrids)	Characters									
	Plant height (cm)	Peduncul e length (cm)	Tillers per plant	Spike length	Spikelets per pike	Grains per spike	Seed index	Grain yield per plant	Biological yield per plant	Harvest index
	Parents									
Sunhari	81.00	33.26	4.75	10.67	17.69	51.85	30.75	6.19	15.35	40.59
PBG-02	81.73	33.50	5.25	12.97	19.10	58.29	37.08	7.70	18.03	43.16
Sarsabz	102.27	39.56	5.22	12.40	21.70	63.00	26.67	7.53	21.31	35.82
TD-1	57.50	25.88	5.63	10.28	15.03	49.38	31.17	6.22	16.07	38.62
TJ-83	68.28	26.00	4.91	11.88	17.97	55.97	24.16	4.88	14.32	33.94
Moomal	80.58	37.75	4.40	11.23	16.77	63.04	27.50	4.77	13.77	35.76
Average	78.56	32.66	5.03	11.41	18.04	56.92	29.56	6.22	16.48	37.98
	F <sub>2</sub> hybrids									
TJ-83 x TD-1	84.58	37.97	4.85	12.58	20.70	58.99	34.17	7.35	18.83	39.07
PBG-02 x TD-1	82.97	34.47	5.12	13.22	19.45	59.70	37.50	8.34	20.95	39.80
TJ-83 x Moomal	87.97	36.90	4.85	13.85	20.62	55.37	34.17	8.82	18.77	46.97
Moomal x TD-1	89.75	37.27	5.53	13.42	20.77	64.07	35.83	9.52	22.05	43.17
TD-1 x Sarsabz	76.65	33.72	5.43	12.18	17.47	55.37	32.00	7.37	16.30	45.21
Sarsabz x Moomal	82.77	38.20	5.33	13.61	20.82	63.20	31.50	7.72	19.35	39.88
TJ-83 x Sarsabz	90.47	39.69	5.66	12.70	19.62	60.10	32.92	8.20	21.49	38.18
Sunhari x TD-1	83.95	37.11	5.93	12.01	19.18	57.87	30.41	8.52	21.55	39.52
Average	84.89	36.92	5.34	12.95	19.83	59.33	33.56	8.23	19.91	41.48
LSD (5%)	2.80	1.31	0.28	0.53	0.90	3.68	2.71	1.21	2.76	3.54

## Genetic parameters of F<sub>2</sub> populations

### Plant height

Table 3 shows plant height inherited, phenotype, environmental variation, heritability estimates and genetic progress. The results further revealed that the F<sub>2</sub> population exhibited a broader range of phenotypes ( $\sigma^2_p = 62.36$  to  $313.61$ ) and genetic variation ( $\sigma^2_g = 35.88$  to  $309.86$ ) and estimated the moderate to highly heritable nature of the trait. The highest heritability with the greatest genetic progression was observed in the offspring TJ-83 x TD-1 (98.80%, 24.50), followed by Sunhari x TD-1 (98.76%, 23.85), but at the crossover Moomal x The lowest heritability was observed in TD-1 (57.54%, 6.36). On the basis of individual populations, their phenotypic differences are very close to their respective genotype differences, so the recorded heritability estimates range from 57.54% to 98.8%.

**Table 3** Heritability estimates and genetic advance of eight F<sub>2</sub> populations of bread wheat for Plant height

F <sub>2</sub> population	Genotypic Variance ( $\sigma^2_g$ )	Phenotypic Variance ( $\sigma^2_p$ )	Environmental Variance ( $\sigma^2_e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	309.86	313.61	3.75	98.80	24.50
PBGST-2 x TD-1	172.97	191.73	18.76	90.21	17.49
TJ-83 x Moomal	115.47	139.12	23.65	83.00	13.71
Moomal x TD-1	35.88	62.36	26.48	57.54	6.36
TD-1 x Sarsabz	154.72	171.86	17.14	90.03	16.52
Sarsabz x Moomal	156.23	173.37	17.14	90.12	16.61
TJ-83 x Sarsabz	182.02	196.32	14.31	92.71	18.19
Sunhri x TD-1	293.83	297.51	3.68	98.76	23.85

**Peduncle length**

Table 4 describes the genetic progression ( $\sigma^2_g$ ), phenotypic variance ( $\sigma^2_p$ ), environmental variance ( $\sigma^2_e$ ), heritability estimates (b.s.), and genetic progression of peduncle length. The results showed that the F<sub>2</sub> population expressed a broader genotype variance ( $\sigma^2_g$  = 8.57 to 55.64). The F<sub>2</sub> population also expressed a moderate to high heritability estimate for this feature. The maximum heritability and the highest hereditary progression were estimated from the cross TJ-83×Sarsabz (89.57%, 9.88), while the minimal heritability was observed in the cross Sarsabz x Moomal (47.45%). However, the lowest genetic progression was calculated from the progeny Moomal x TD-1 (2.88).

**Table 4** Heritability estimates and genetic advance of eight F<sub>2</sub> populations for of bread wheat for Peduncle length

F <sub>2</sub> population	Genotypic Variance ( $\sigma^2_g$ )	Phenotypic Variance ( $\sigma^2_p$ )	Environmental Variance ( $\sigma^2_e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	32.95	39.56	6.60	83.30	7.34
PBGST-2 x TD-1	16.79	25.30	8.52	66.33	4.67
TJ-83 x Moomal	23.73	27.49	3.75	86.34	6.34
Moomal x TD-1	8.57	17.32	8.75	49.50	2.88
TD-1 x Sarsabz	25.89	37.36	11.47	69.30	5.93
Sarsabz x Moomal	10.36	21.82	11.47	47.45	3.10
TJ-83 x Sarsabz	55.64	62.12	6.48	89.57	9.88
Sunhri x TD-1	50.27	57.26	6.99	87.79	9.30

**Tillers per plant**

Genetic parameters such as phenotype ( $\sigma^2_p$ ), genotype ( $\sigma^2_g$ ), environmental ( $\sigma^2_e$ ) variance, heritability estimate (bs) and genetic progression of each plant tiller are shown in Table 5. The results showed that F<sub>2</sub> hybrids exhibited different phenotypic variation ranges ( $\sigma^2_p$  = 17.32 to 62.12). Low to moderate heritability was observed for tillering of each plant. The highest heritability with the greatest genetic progression was measured in F<sub>2</sub> progeny like TJ-83 x Sarsabz (55.64%, 1.94). However, minimal heritability with low genetic progression was observed in the cross Sarsabz x Moomal (22.30%, 0.62). Phenotypic variation in the F<sub>2</sub> population is usually twice as high as its corresponding genetic variation, so almost all populations have lower heritability's.

**Table 5** Heritability estimates and genetic advance of eight F<sub>2</sub> populations of bread wheat for Tillers per plant

F <sub>2</sub> population	Genotypic Variance ( $\sigma^2_g$ )	Phenotypic Variance ( $\sigma^2_p$ )	Environmental Variance ( $\sigma^2_e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	1.24	3.82	2.58	32.43	0.89
PBGST-2 x TD-1	1.68	3.94	2.25	42.81	1.19
TJ-83 x Moomal	1.38	3.66	2.28	37.66	1.01
Moomal x TD-1	1.71	4.29	2.58	39.78	1.15

TD-1 x Sarsabz	1.03	4.08	3.05	25.33	0.72
Sarsabz x Moomal	0.87	3.92	3.05	22.30	0.62
TJ-83 x Sarsabz	3.44	6.19	2.74	55.64	1.94
Sunhri x TD-1	3.48	6.37	2.89	54.66	1.93

### Spike length

In the case of spike length Table 6, the genotype, phenotype and environmental variation range were  $\sigma^2g = 1.687$  to  $5.60$ ,  $\sigma^2p = 2.92$  to  $6.93$  and  $\sigma^2e = 1.21$  to  $1.40$ , respectively. Crossover TJ-83×TD-1 showed the highest heritability (80.79%), which was associated with higher genetic progression (2.98), followed by TJ-83×Moomal (68.96%) and genetic progression of 2.05. However, the lowest heritability (56.13%) was estimated by the progeny Moomal x TD-1, and the lowest genetic progression was estimated by the progeny TD-1×Sarsabz (1.37).

**Table 6** Heritability estimates and genetic advance of eight  $F_2$  populations of bread wheat for Spike length

$F_2$ population	Genotypic Variance ( $\sigma^2g$ )	Phenotypic Variance ( $\sigma^2p$ )	Environmental Variance ( $\sigma^2e$ )	Heritability (b.s.%)	Genetic advance
TJ-83 x TD-1	5.60	6.93	1.33	80.79	2.98
PBGST-2 x TD-1	2.66	3.87	1.21	68.70	1.89
TJ-83 x Moomal	3.11	4.51	1.40	68.96	2.05
Moomal x TD-1	1.80	3.21	1.41	56.13	1.41
TD-1 x Sarsabz	1.68	2.92	1.25	57.37	1.37
Sarsabz x Moomal	2.70	3.94	1.25	68.38	1.90
TJ-83 x Sarsabz	2.23	3.47	1.24	64.28	1.68
Sunhri x TD-1	1.91	3.01	1.10	63.45	1.54

### Spikelets per pike

High and moderate heritability of spikelets per year was observed. The genotypes ( $\sigma^2g = 1.72$  to  $10.64$ ), the phenotype ( $\sigma^2p = 3.36$  to  $13.03$ ) and the environmental variance ( $\sigma^2e = 1.64$  to  $3.92$ ) were recorded and listed in Table 7. High heritability (81.68%) showed genetic progression by crossover TJ-83 x TD-1 (4.13). However, the lowest heritability is estimated by the offspring Sunhari x TD-1 (40.31). The minimum genetic progression is estimated to be cross TD-1 x Sarsabz (1.20). Two populations, TJ-83×TD-1 and TJ-83×Moomal, which express very close genetic and phenotypic variations, provide higher estimates of heredity (above 80%). A population with a low heritability variance for its phenotypic variation recorded a low heritability estimate for spikelet spike-1.

**Table 7** Heritability estimates and genetic advance of eight  $F_2$  populations of bread wheat for Spikelets per pike

$F_2$ population	Genotypic Variance ( $\sigma^2g$ )	Phenotypic Variance ( $\sigma^2p$ )	Environmental Variance ( $\sigma^2e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	10.64	13.03	2.39	81.68	4.13
PBGST-2 x TD-1	3.71	6.01	2.30	61.74	2.12
TJ-83 x Moomal	10.26	12.58	2.32	81.59	4.05
Moomal x TD-1	2.96	6.15	3.19	48.17	1.67
TD-1 x Sarsabz	1.78	4.29	2.51	41.47	1.20
Sarsabz x Moomal	4.15	6.66	2.51	62.33	2.25
TJ-83 x Sarsabz	1.72	3.36	1.64	51.23	1.31
Sunhri x TD-1	2.22	5.51	3.29	40.31	1.32

### Grains per spike

The low to moderate heritability of the number of grains per panicle in the  $F_2$  population was estimated (table 8). The variance of genotype ranged from  $\sigma^2g=30.77\sim96.89$ , the variance of phenotype was  $\sigma^2p=121.27\sim204.95$ , and the environmental variance was  $\sigma^2e= 71.30\sim164.78$ . The  $F_2$  from the cross TJ-83×TD-1 represents the largest but moderate heritability (57.61%), with the highest

genetic progress (10.46), followed by TD-1×Sarsabz, the heritability rate is 47.44%, and the genetic progression is 9.31. . However, TJ-83×Moomal (19.60%) recorded minimal heritability, but the lowest genetic progression was observed in cross-PBGST-02×TD-1 (3.64). Almost all F<sub>2</sub> populations provide low heritability estimates because environmental differences are greater than their genotypic differences and the boundaries of genetic differences ultimately lead to a reduction in heritability estimates.

**Table 8** Heritability estimates and genetic advances of eight F<sub>2</sub> populations of bread wheat for Grains per spike

F <sub>2</sub> population	Genotypic variance ( $\sigma^2_g$ )	Phenotypic variance ( $\sigma^2_p$ )	Environmental variance ( $\sigma^2_e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	96.89	168.19	71.30	57.61	10.46
PBGST-2 x TD-1	30.77	139.74	108.97	22.02	3.64
TJ-83 x Moomal	40.17	204.95	164.78	19.60	3.93
Moomal x TD-1	44.65	203.08	158.43	21.99	4.39
TD-1 x Sarsabz	93.23	196.51	103.28	47.44	9.31
Sarsabz x Moomal	62.33	165.61	103.28	37.64	6.78
TJ-83 x Sarsabz	57.93	167.55	109.62	34.57	6.27
Sunhri x TD-1	36.31	121.27	84.96	29.94	4.62

### Seed index

The characteristic seed index represents a high to medium heritability estimate (table 9). The genetic variance ranged from  $\sigma^2_g$  = 11.46 to 29.94; the phenotypic variance was  $\sigma^2_p$  = 17.60 to 32.40, and the environmental variance was  $\sigma^2_e$  = 2.18 to 12.50. The highest heritability was tested in crossover Moomal x TD-1 (92.44%) and maximum genetic progression (7.37) and crossover Sunhari x TD-1 (90.49%). However, the minimal heritability comes from the offspring of the cross TJ-83×Sarsabz (45.48%) and the lowest genetic progression (3.05). Populations with large genetic differences provide relatively more genetic progression, indicating that the added genes control the seed index in these offspring.

**Table 9** Heritability estimates and genetic advance of eight F<sub>2</sub> populations of bread wheat for Seed index (1000-grain wt.)

F <sub>2</sub> population	Genotypic Variance ( $\sigma^2_g$ )	Phenotypic Variance ( $\sigma^2_p$ )	Environmental Variance ( $\sigma^2_e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	11.46	17.60	6.14	65.12	3.82
PBGST-2 x TD-1	12.49	17.60	5.11	70.97	4.17
TJ-83 x Moomal	25.92	32.40	6.48	80.01	6.38
Moomal x TD-1	29.94	32.39	2.45	92.44	7.37
TD-1 x Sarsabz	14.20	22.67	8.47	62.64	4.17
Sarsabz x TD-1	16.27	24.74	8.47	65.77	4.58
TJ-83 x Sarsabz	10.43	22.92	12.50	45.48	3.05
Sunhri x Moomal	20.73	22.91	2.18	90.49	6.06

### Grain yield per plant

A low to high heritability estimate was observed for each plant's grain yield (Table 10). Genotype differences ranged from 2.13 to 13.40, phenotypic differences ranged from 9.86 to 18.19, and environmental differences ranged from 4.79 to 10.93. Low heritability estimates were recorded because the genotype differences in the F<sub>2</sub> population were much lower than their respective phenotypic variations. However, the highest heritability (4.40) was observed in the progeny TJ-83 x Moomal (73.67%) associated with the greatest genetic progression. The minimum heritability was estimated in the offspring TJ-83 x TD-1 (21.56%) and minimal genetic progression (0.95). In general, almost all F<sub>2</sub> populations exhibit low heritability, thus indicating that environmental differences are not effectively controlled.



**Table 10** Heritability estimates and genetic advance of eight F<sub>2</sub> populations of bread wheat for Grain yield per plant

F <sub>2</sub> population	Genotypic Variance ( $\sigma^2_g$ )	Phenotypic Variance ( $\sigma^2_p$ )	Environmental Variance ( $\sigma^2_e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	2.13	9.86	7.73	21.56	0.95
PBGST-2 x TD-1	4.00	13.67	9.67	29.27	1.51
TJ-83 x Moomal	13.40	18.19	4.79	73.67	4.40
Moomal x TD-1	7.70	15.00	7.30	51.36	2.78
TD-1 x Sarsabz	5.30	15.69	10.39	33.79	1.87
Sarsabz x Moomal	7.04	17.43	10.39	40.37	2.36
TJ-83 x Sarsabz	8.04	15.93	7.88	50.49	2.82
Sunhri x TD-1	7.99	16.90	8.91	47.28	2.72

### Biological yield per plant

The F<sub>2</sub> progeny of the biological yield of each plant was estimated to have a moderate to low heritability (Table 11). The genetic variance ranged from 8.32 to 67.14; the phenotypic differences ranged from 68.05 to 118.46, and the environmental differences ranged from 33.27 to 65.20. The highest heritability (56.68%) and the highest genetic progression (8.64) were observed after TJ-83×Sarsabz crosses, followed by TJ-83×Moomal (51.11%). However, the minimum heritability was estimated to be cross Sarsabz x TD-1 (11.32%) and lowest genetic progression (1.36). Except for a small number of people, most of them estimate that the genetic yield of per plant is low. These results indicate that selection can be postponed to increase the biomass production of per plant until later segregation.

**Table 11** Heritability estimates and genetic advance of eight F<sub>2</sub> populations of bread wheat for Biological yield

F <sub>2</sub> population	Genotypic Variance ( $\sigma^2_g$ )	Phenotypic Variance ( $\sigma^2_p$ )	Environmental Variance ( $\sigma^2_e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	32.75	76.99	44.24	42.54	5.23
PBGST-2 x TD-1	22.11	76.56	54.45	28.87	3.54
TJ-83 x Moomal	34.78	68.05	33.27	51.11	5.90
Moomal x TD-1	26.81	73.96	47.15	36.25	4.36
TD-1 x Sarsabz	9.09	74.29	65.20	12.23	1.48
Sarsabz x Moomal	8.32	73.52	65.20	11.32	1.36
TJ-83 x Sarsabz	67.14	118.46	51.31	56.68	8.64
Sunhri x TD-1	44.27	92.93	48.66	47.63	6.43

### Harvest index

Observe the moderate heritability estimates for the harvest index as shown in Table 12. The variance range is recorded in the following manner. Genotypes ranged from 8.05 to 85.41; phenotypes ranged from 74.90 to 151.37, and the environment ranged from 60.20 to 75.49. The highest heritability (56.42%) was shown by crossover TJ-83 x Moomal and maximum genetic progression (9.72), while the minimum heritability (9.97%) was represented by cross Sarsabz x TD-1 with the lowest genetic progression (1.25).

**Table 12** Heritability estimates and genetic advance of eight F<sub>2</sub> populations of bread wheat for Harvest index

F <sub>2</sub> population	Genotypic Variance ( $\sigma^2_g$ )	Phenotypic Variance ( $\sigma^2_p$ )	Environmental Variance ( $\sigma^2_e$ )	Heritability (b.s. %)	Genetic advance
TJ-83 x TD-1	18.90	82.34	63.45	22.95	2.92
PBGST-2 x TD-1	1.82	79.03	60.20	23.82	2.96
TJ-83 x Moomal	85.41	151.37	65.96	56.42	9.72
Moomal x TD-1	9.46	74.90	65.44	12.63	1.53
TD-1 x Sarsabz	32.72	105.43	72.71	31.04	4.46



Sarsabz x Moomal	8.05	80.76	72.71	9.97	1.25
TJ-83 x Sarsabz	9.82	83.06	73.24	11.83	1.51
Sunhri x TD-1	14.84	90.33	75.49	16.43	2.19

## 4. DISCUSSION

### Plant height

Most researchers believe that plant height is a polygenic trait due to the genetic pattern in the isolated population. Among wheat, semi-dwarf plants with high productivity are more desirable. The results in Table 2 indicate that pro-Sarsabz produced the tallest plant (102.27 cm) compared to the other parental lines and F<sub>2</sub> progeny, while TD-1 produced the shortest plant (57.50 cm). In the cross, the offspring TJ-83 x Sarsabz produces the tallest plant, 90.47 cm long, while the shortest plant is recorded by TD-1 x Sarsabz (76.65 cm). The results shown in Table 3 indicate that the maximum (98.80%) of the heritability associated with high plant height (24.50) of plant height is represented by the offspring TJ-83 x TD-1. However, other F<sub>2</sub> progeny showed moderate to high heritability estimates and considerable genetic gain. Our results are consistent with the others findings [3,17,18,19] they also studied genetic parameters and recorded higher genotypic variability; medium to high heritability values and plant height greater inheritance The combination of progress. They also observed highly significant differences between parents and hybrids. Existing results with higher heritability estimates and significant genetic progression indicate that plant height is primarily controlled by additive genes, so direct selection may be effective in isolated generations. Furthermore, the results indicate that offspring with ideal genetic parameters TJ-83 x TD-1, Sunhari x TD-1, TJ-83 x Sarsabz, PBG-02 x TD-1, Sarsabz x Moomal and TD-1 x Sarsabz may be Breeding materials are selected for selection to increase the plant height of subsequent generations.

### Peduncle length

Inflorescence length is a part of a wheat plant that is measured from the top node to the base of the ear. The average performance shown in Table 2 indicates that among parents, the longest peduncle length (39.56 cm) was produced by Sarsabz; while the parental TD-1 measured the shortest peduncle length of 25.88 cm. In the F<sub>2</sub> progeny, TJ-83 x Sarsabz produced the longest peduncle length (39.69 cm) and the shortest TD-1 x Sarsabz (33.72). The results of the genetic parameters shown in Table 4 indicate that the offspring exhibit moderate to high genetic and genetic progression. The highest heritability associated with greater genetic progression ( $h^2 = 89.57\%$ ) ( $GA = 9.88$ ) was expressed by the progeny TJ-83 x Sarsabz. The current results are consistent with the results of other researchers those also recorded the high heritability of inflorescence length [20,21,22].

### Tillers per plant

Tiller is the main yield component and has a direct impact on food production, so this improvement in characteristics will ultimately increase food production. Regarding the average performance, the parental line TD-1 produced the maximum number of tillers per plant (5.66), followed by PBG-02 (5.25), while the parent Moomal produced the smallest tiller plant-1 (4.40). In the F<sub>2</sub> offspring, crossover Sunhari x TD-1 recorded the maximum number of tillers per plant (5.25), while the smallest tiller per plant (4.85) was produced by TJ-83 x Moomal and TJ-83 x TD-1. The results of the genetic parameters showed that most of the F<sub>2</sub> progeny showed a considerable amount of genetic variability and low to moderate heritability estimates, but the offspring from the TJ-83xSarsabz cross showed the highest heritability ( $h^2 = 55.64\%$ ). ), with greater genetic progression ( $GA = 1.94$ ), while minimal heritability ( $h^2 = 22.30$ ) was expressed by the general advancement of the offspring Sarsabz x Moomal and 0.62. The results generally indicate that F<sub>2</sub> progeny from TJ-83 x Sarsabz and Sunhari x TD-1 hybrids may be selected from further progeny to improve selective propagation of individual tillers. Similar to our results, significant genetic variation and low to moderate heritability estimates for tillering of each plant were also observed [3,18,23].

### Spike length

On average, among the parents, PBG-02 exhibited maximum spike length (12.97cm), while minimum spike length was measured from parent TD-1 (10.28cm). Among the F<sub>2</sub> populations, TJ-83 x Moomal produced longer spikes (13.85cm) narrowly followed by Sarsabz x Moomal (13.61cm). However, progenies from cross TJ-83 x TD-1 displayed highest heritability ( $h^2 = 80.94\%$ ) coupled with maximum genetic advance ( $GA = 2.98$ ). The other F<sub>2</sub> progenies like TJ-83 x Moomal ( $h^2 = 68.96\%$ ), PBG-02 x TD-1 ( $h^2 = 68.70\%$ ) and Sarsabz x Moomal ( $h^2 = 68.38\%$ ) nonetheless exhibited higher heritability estimates. Present results are in conformity with those who also observed higher heritability percentage for spike length and controlled by additive genetic factors [11,17,22,24,25].

### Spikelets per spike

The spikelets of each ear steadily promote the grain yield of wheat. Therefore, plant breeders and researchers suggest that spikelets per ear are indeed a good standard for selecting high-yielding wheat varieties. The average performance of the genotypes shown in Table 2 indicates that in the parent, the largest spikelets (21.70) per ear were produced by Sarsabz. In the  $F_2$  descendants, Sarsabz x Moomal (20.82) is followed by Moomal x TD-1 (20.77) and TJ-83 x TD-1 (20.70), recording the maximum number of spikelets per ear. The results of the genetic parameters shown in Table 7 indicate that several  $F_2$  progeny exhibit moderate to high heritability estimates and genetic progression. However, the highest heritability ( $h^2 = 81.68\%$ ) associated with greater genetic progression ( $GA = 4.13$ ) was reached by post-representation from cross TJ-83 x TD-1. These results indicate that progeny TJ-83 x TD-1 and TJ-83 x Moomal with the desired genetic parameters can be considered as valuable breeding materials for selecting the desired plants in further progeny, thereby improving the trait. Our findings are consistent with the findings of who observed a moderate to high heritability of spikelets per ear [11, 17].

### Cereal spike-1

The number of grains per panicle is the main yield component, so an increase in the number of grains per panicle will eventually increase the yield of wheat. Based on the average performance, the mother Moomal calculated the maximum number of grains per ear (63.04), followed by Sarsabz (63.00). The genetic parameters shown in Table 8 indicate that most offspring express a moderate to low percentage of heredity in a broad sense, indicating significant genetic variability. The offspring from the TJ-83xTD-1 crossover showed the highest heritability (57.61%) and higher genetic progression (10.46) in a broad sense. Furthermore, these results indicate that the progeny of TJ-83 x TD-1 and TD-1 x Sarsabz may be separate populations to improve the selection of kernel per panicle. Others also noted the low-medium heritability of the number of grains per panicle [22,26,27,28].

### Seed index (thousand grain weights)

The seed index is a multi-gene trait that has a large impact on wheat grain yield. The parental average of the seed index ranged from 24.16 to 37.08 g, while the average of the  $F_2$  progeny ranged from 30.41 to 37.50 g. The results of the genetic parameters representing the seed index in Table 9 show that almost all  $F_2$  progeny show a moderate to high heritability estimate, but the broadest heritability in the broadest sense ( $h^2 = 92.44\%$ ) and maximum genetic progression ( $GA = 7.37$ ) behaved as a descendant. Moomal x TD-1 is followed by Sunhari x Moomal ( $h^2 = 90.49\%$ ,  $GA = 6.06$ ). The results indicate that  $F_2$  progeny from hybrid Moomal x TD-1, Sunhari x Moomal and TJ-83 x Moomal may be preferred for selection to improve the seed index of wheat. Former workers, their research yielded similar results [11,17,19,25].

### Grain yield per plant

Yield is still the most important of all characteristics in any crop variety. The yield per plant is largely determined by the four yield components. Spike length, spikelet spike-1, grain spike-1 and seed index. Based on the average performance shown in Table 2, the results indicate that the parent PBG-02 produced a maximum grain yield per plant (7.70 g) followed by Sarsabz (7.53 g). In  $F_2$  offspring, Moomal x TD-1 showed the highest average (9.52 g). The results of the genetic parameters shown in Table 10 indicate that the offspring show a low to high heritability estimate and genetic progression. The maximum heritability associated with greater genetic progression ( $h^2 = 73.67\%$ ) ( $GA = 4.40$ ) was reached by the post-representation from the cross TJ-83 x Moomal. These results indicate that progeny from hybrid TJ-83xMoomal, Moomal x TD-1 and TJ-83xSarsabz with the desired genetic parameters can be considered for selection in further progeny to improve Grain yield per plant. Similar results were observed [17,18,25,26,28].

### Biological yield per plant

Based on the average performance, pro-Sarsabz gave the maximum biomass yield per plant (21.31g), while in the  $F_2$  progeny, the highest grade was Moomal x TD-1 (22.05g). The genetic parameters listed in Table 11 confirm that most offspring express a low heritability estimate in a broad sense, so the choice of biological yield can be made in subsequent segregation generations. The offspring from the TJ-83xSarsabz cross showed the highest heritability (56.68%) in the broadest sense, with the greatest genetic progression (8.64). Other  $F_2$  offspring such as TJ-83xMoomal ( $h^2 = 51.55\%$ ) and Sunhari x TD-1 ( $h^2 = 47.63\%$ ) also showed the highest but moderate heritability estimates. These progenies can be used as potential separation materials for selection to increase the biological yield of each plant. The current results are consistent with the results of other researcher they also observed a moderate heritability of individual plant biomass [19].

## Harvest index

The harvest index is also a multi-gene trait that has an indelible effect on wheat grain yield. The parental average of the harvest index ranged from 33.94% to 43.16%, while the average of the F<sub>2</sub> progeny ranged from 38.18% to 46.97% (Table 2). The results of the genetic parameters representing the harvest index shown in Table 12 show that almost all F<sub>2</sub> progeny show low to moderate heritability estimates, but broadly the highest heritability ( $h^2 = 56.42\%$ ) and maximum genetic progression ( $GA = 9.72$ ) The performance is the offspring TJ-83 x Moomal, while Sarsabz x TD-1 expresses the lowest heritability ( $h^2 = 9.97\%$ ), which is also associated with minimal genetic progression (1.25). Our findings are consistent with the findings of other researcher they also observed a low to moderate heritability of the seed index in a broad sense [19].

## 5. CONCLUSION

The study generally indicates genetic variation between the genotypes studied. Most of them have high heritability and genetic, so direct selection have good results for these populations.

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**Data and materials availability:** All data associated with this study are present in the paper.

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